

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: August 22, 2003, 13:49:06 ; Search time 30 Seconds

(without alignments)
4380.584 Million cell updates/sec

Title: US-09-745-506-74

Perfect score: 2789

Sequence: 1 GCGATGTTACTTACTGCTGCT.....TCGTTTACTTAACATTCAA 1553

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

-MODEL-framer.n2p.model -DEV-x1p
-O/cgn2.1/USPRO.spool/US09745506/runat_22082003_132711_10806/app_query.fasta.1.1735
-DB-issued_patents_AA -OPMT-fastn -SUFFIX-n2p.ra1 -MINMATCH-0.1 -LOOPEL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-biosum62 -TRANS-human4.0.cd1
-LIST-45 -DOCALLIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTPM-pto -NORM-ext -HEADSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09745506.ecgn.1.1.38.runat.22082003_132711_10806 -NCPD-6 -ICPD-3
-NO_MMAP -LARGEQUERY -NIG_SCORES-0 -WAIT -DSRBLCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAEXT-0.5 -DELOP-6 -DELEXT-7

Database :

- 1: Issued_Patents_AA.*
- 2: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*
- 3: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*
- 4: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*
- 5: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*
- 6: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	321.5	11.5	378	4	US-09-107-532A-4742
2	305	10.9	367	4	US-09-134-001C-3678
3	106	3.8	256	4	US-09-252-991A-24651
4	104.5	3.7	473	4	US-09-534-899-4
5	103.5	3.7	262	4	US-09-328-352-4482
6	103	3.5	673	4	US-09-146-053-2
7	97.5	3.5	509	4	US-09-252-991A-28680
8	97	3.5	588	4	US-09-328-352-7994
9	96.5	3.5	493	4	US-10-002-593-10
10	96	3.4	503	3	US-08-911-853-7
11	96	3.4	503	3	US-09-479-409-7
12	96	3.4	503	4	US-09-479-453-7

c	13	96	3.5	724	4	US-09-984-890-2	Sequence 2, Appl1
	14	95	3.4	638	4	US-08-681-151-3	Sequence 3, Appl1
	15	95	3.4	804	4	US-09-134-001C-5218	Sequence 5218, Ap
	16	95	3.4	1172	1	US-08-313-2888-19	Sequence 19, Appl
	17	94.5	3.4	251	4	US-09-198-452A-156	Sequence 156, App
	18	93.5	3.4	488	4	US-09-252-991A-31307	Sequence 31307, A
	19	93	3.4	787	4	US-09-252-991A-28939	Sequence 28939, A
	20	92	3.4	2930	4	US-09-417-821A-2	Sequence 2, Appl1
	21	91	3.3	501	2	US-08-969-630-4	Sequence 4, Appl1
	22	91	3.3	735	4	US-09-134-001C-3440	Sequence 3440, Ap
	23	90.5	3.3	417	4	US-09-252-991A-23413	Sequence 23413, A
	24	90.5	3.3	1537	4	US-09-376-330-2	Sequence 2, Appl1
	25	90	3.2	281	4	US-09-252-991A-25970	Sequence 25970, A
	26	90	3.2	595	4	US-09-328-352-4432	Sequence 4432, Ap
	27	90	3.2	1058	4	US-09-328-352-4276	Sequence 4276, Ap
	28	89.5	3.2	1651	3	US-09-540-245A-18	Sequence 18, Appl
	29	89.5	3.2	2512	2	US-08-801-263A-9	Sequence 9, Appl1
	30	89.5	3.2	2512	3	US-09-102-248-9	Sequence 9, Appl1
	31	89.5	3.2	2512	4	US-09-367-764-9	Sequence 9, Appl1
	32	89	3.2	907	4	US-09-170-496D-264	Sequence 264, App
	33	89	3.2	907	4	US-09-170-496D-278	Sequence 278, App
	34	89	3.2	951	4	US-09-328-352-4456	Sequence 4456, Ap
	35	88.5	3.2	405	2	US-08-222-719-2	Sequence 2, Appl1
	36	88.5	3.2	405	2	US-08-470-925-2	Sequence 2, Appl1
	37	88.5	3.2	405	2	US-08-471-613-2	Sequence 2, Appl1
	38	88.5	3.2	405	5	PCT-US93-10443-2	Sequence 2, Appl1
	39	88.5	3.2	405	2	US-08-702-598-2	Sequence 2, Appl1
	40	88.5	3.2	514	4	US-09-328-352-6997	Sequence 6997, Ap
	41	88.5	3.2	800	3	US-08-776-263-3	Sequence 3, Appl1
	42	88	3.2	1154	4	US-09-134-001C-3428	Sequence 3428, Ap
	43	87.5	3.1	355	4	US-09-134-001C-5391	Sequence 5391, Ap
	44	87.5	3.1	498	3	US-09-134-607A-19	Sequence 19, Appl
	45	87.5	3.2	609	3	US-08-927-219-129	Sequence 129, App

ALIGNMENTS

RESULT 1
US-09-107-532A-4742
Sequence 4742, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arlindo, Pamela Denek
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

```

; INFORMATION FOR SEQ ID NO: 4742:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 378 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
; FEATURE:
;   NAME/KEY: misc.feature
;   LOCATION: (B) LOCATION 1...378
; SEQUENCE DESCRIPTION: SEQ ID NO: 4742:
US-09-107-532A-4742

Alignment Scores:
Pred. No.:      3,19e-25      Length:      378
Score:          321.50       Matches:      103
Percent Similarity: 45.19%   Conservative: 80
Best Local Similarity: 25.43% Mismatches: 133
Query Match:    11.53%      Indels:      89
DB:              4          Gaps:        17

US-09-745-506-74 (1-1553) x US-09-107-532A-4742 (1-378)

OY      230 TCCTCCGCTTCCTTCATGATGTAAGGCTCTCTTCTCTTCCTGAATGACTTTGCAATCC 289
DB      9 SerGlyArgThrPhe-----IleGlnLysPheGluSerTyrCysPro 22
OY      290 CTCGCTGTTGGTGAGTTGGGACAAATGTGGATTA-----CTGTGGAACA 337
DB      23 GlnTrpLeuAlaGluGlnGlyAspProValGlyLeuHisIleGlyThrLeuAspLysPro 42
OY      338 AGCCACCCACATCTGTAATAACTCTTCTGACCAATGACTGACTGAGAAAGTATG 397
DB      43 -----IleGlnArgValIleMetThrLeuAspValArgProGluVal 57
OY      398 GAGGAGTGCTGCAAAAAGAGCAGACCTCATTTCTCTTACCATCCGCTATCTCCGA 457
DB      58 GluGlnAlaIleLysLysIleAspLeuIleAlaLysHisAspProIlePheArg 77
OY      458 CCCATGAGCCGATACCTGGAACACATGAGAGCCGCTGGTATCCGGCTCTGGAG 517
DB      78 ProValLysArgLeuValThrAspGlnProGlnGluLysMetTyrAlaAspLeuLys 97
OY      518 AACAGAGTGGTATCTACTCTCTCATACAGCCTATGATGCTGCCGCCAGGCGCTCAAC 577
DB      98 HisAspIleAlaValTyrAlaIleHisThrAsnMetAspIleIleTrpAspLysLeuAsn 117
OY      578 AACTGGTGGGTAAGGCGCTGGA-----GCTTGACCTCCAGGCC 619
DB      118 AspTrpPheCysGluLeuLeuGlyIleGluValGluSerTyrLeuValLysThrHisGlu 137
OY      620 ATACATCTCTCCAAAGCTCCCAACTACCTACAGAGGAAACACCGAGTAGAATTAAC 679
DB      138 IleHisTyrLysLysLeuAlaValTyr-----ValPro 148
OY      680 GTTAATCAACCCCAAGACCTGGACAAATCATGTCGTGCAAGTAAGA----- 727
DB      149 ValAspHisAlaGlnLysMetArgGluValLeuAlaIleAlaGlyAlaGlyThrGlnGly 168
OY      728 ---ATTGACGGTGTTCGTCACTCTTTTCT----- 757
DB      169 AspTyrThrGlyThrSerPheThrSerIleGlyHisGlyArgPheThrProGluAlaGly 188
OY      758 -----GTTAGACCTGTAATGAGCAACAACGAGATTAACTGAATGT 802
DB      189 AlaGlnProAlaIleGlyLysValGlyLysThrGln----- 201
OY      803 ACTCAAGAGGCTTTGATCAGAGTGTGATTTTCTTCCCGAACAAACACTTATGAG 862
DB      202 ValGlnGluAlaLysValGluValIleLeuProGluTrpIleGluLysGlnValIleGln 221

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OY      863 AAGACG-----GAATTTGTCTACAGGAGAG 889
DB      222 AlaMetArgSerAlaHisProGlyGluIleProAlaTyrAspLeuPheAlaIleAspL 241
OY      890 CCTTGGCTTTACATACGAAATGGAGCGTTATGCAACATGGAATCTGTCTCCGT 949
DB      242 ProValGluMetPhe--GlyLeuGlyArgValGlyGluLeuProGlnGluIlePheIle 260
OY      950 GCAACCATGATGATGCAATAAAGACACCTAAACATATGCTATATCGCTAGCCCT 1009
DB      261 GluAlaPheValGluGlnValLysGluAlaPheGlnLeuAspArgLysLeuAlaIleVal 279
OY      1010 GGGGTGGGAGAACCTTAAGCTTCACATCAAAAGCTGGCCGTGTGCTGGTTCGG 1069
DB      280 --GlnProLysAsnAlaLysSerSerValLysArgIleAlaIleCysGlyGlySerGly 298
OY      1070 AGCAGCGTTG---CAGCGGTG-----GAGCGTGACCTTTCCCTACAGGAGAGATG 1120
DB      299 GluLysPheTyrProGlnAlaIleAlaGlnArgAlaAspValTyrIleThrGlyAspIle 318
OY      1121 TCCCATCATGATACCTTTGATGCTGCTCCCAAGGAATTAATGTCATC----- 1168
DB      319 TyrTyrHisThrAlaHisAspMetGlnSerAlaGlyLeuIleAlaIleAspProGlyHis 338
OY      1169 -----CTGTGGAACACGACACCTGACAGCGCTTTCTTCTGACCTTGA 1216
DB      339 TyrIleGluSerLeuCysLysGlnArgPheIleGlyLys---PheGluSerTrpLysGln 357
OY      1217 GATATGCGATTCACATCTTGAGAGAT---AAGATTAATTAATTATTCCTACAGAGCTGAC 1273
DB      358 Glu-----GlnAsnTrpAspIleAsnPheValSerGluTrpAsn 371
OY      1274 AGGACCCCTCTTCAAG 1288
DB      372 ThrAsnProPheGln 376

RESULT 2
US-09-134-001C-3678
; Sequence 3678, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; FILE REFERENCE: GTC-007
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3678
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3678

Alignment Scores:
Pred. No.:      1.77e-23      Length:      367
Score:          305.00       Matches:      96
Percent Similarity: 43.54%   Conservative: 76
Best Local Similarity: 24.30% Mismatches: 145
Query Match:    10.94%      Indels:      78
DB:              4          Gaps:        13

US-09-745-506-74 (1-1553) x US-09-134-001C-3678 (1-367)

OY      245 ATGATTTGAAGGCTCTCTCTTCTCTTGAATGACTTGCATCCCTCGTTGCTGAG 304
DB      2 MetLysIleSerGluLeuMetGluValLeuAsnHisValProPheHisGlnAlaGlu 21
OY      305 AGTTGGACATGTGTTGGATTACTGTGTGAACCAAGCCCAACACATCTGTAATACACTC 364

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QY 848 AACAACTTTATGAGAGGAGAAATTCGTACGTGAGAGCCTTGTCTTACATACT 907
::: :
Db 158 ArgAspAlaLeuGlyArg-----GluProLeuLeuValAspAla 170
QY 908 GGAATGGAGCGTTATGCACACGTGATGATTCGTCTCCCTGGACCATGATTGATGCA 967
::: :
Db 171 Gly----- 171
QY 968 ATAAAGACACCTAAATATCATATTCGTTAGCCCTGGGGGTGGGAGAACCTTA 1027
::: :
Db 171 ----- 171
QY 1028 GAGTCTCACTCAAAAGTCGTGGCCCTGTGTGCTGTGGAGACGCTTCTG---CAG 1084
::: :
Db 172 ---GlnProIleArgAlaIleAlaTrpCysThrGlyAlaGlnGlyTrpIleAspGln 190
QY 1085 GGTGTGAGCT-----GACCTTACCTCAGAGTGAATGTCATCATGATGATCTTG 1138
::: :
Db 191 AlaIleAlaIleAlaGlyValAspAlaTrpLeuThrGlyValSerGluGlnThrValHis 210
QY 1139 GATCTGCTCTCCCAAGGAATTAATGTCATCTCTGTGACACACAGCAACTGAACGAGC 1198
::: :
Db 211 SerAlaTrpGluAsnGlyIleSerPheIleAlaIleAlaGlnHisAlaThrGluArgTyr 230
QY 1199 TTCTCTTCTGACCTTCGAGATATCTG 1225
::: :
Db 231 GlyValGlnAlaLeuGlyAspTyrLeu 239

RESULT 4
US-09-934-899-4
; Sequence 4, Application US/09934899
; Patent No. 6537786
; GENERAL INFORMATION:
; APPLICANT: Wang, Siqun
; APPLICANT: Wang, Tao
; APPLICANT: Koffas, Matheos
; APPLICANT: Odum, J. Martin
; APPLICANT: Ye, Rick
; TITLE OF INVENTION: Genes encoding exopolysaccharide production
; FILE REFERENCE: CIL633 US NA
; CURRENT APPLICATION NUMBER: US/09/934, 899
; CURRENT FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Methylobionas 16a
US-09-934-899-4

Alignment Scores:
Pred. No.: 0.0399 Length: 473
Score: 104.50 Matches: 62
Percent Similarity: 32.75% Conservative: 31
Best Local Similarity: 21.83% Mismatches: 88
Query Match: 3.75% Indels: 103
Gaps: 13

US-09-745-506-74 (1-1553) x US-09-934-899-4 (1-473)

QY 41 AGATTGGGTGAGAAAGTCCCTGCG-----CACACAGACAGACGACATAG 88
::: :
Db 202 ArgLeuGlyLysLeuSerAspLeuProArgLeuValSerArgGlnAlaValAspLeuVal 221
QY 89 TGGGACAGGGGTCTGACTCAGACTTAAGTGGCTGTCTGCTGTGTTTCTACTGTCTG 148
::: :
Db 222 TrpValAlaIlePheProGlyAlaSerLeuAlaGluArgValGln----- 235
QY 149 GAAAGGCGCTGAAGTGGACATGAATGAGCATAGATGATGCCACAGACACTGCGGTTT 208
::: :
Db 236 -----HisGluLeuArgHis-----LeuProValSerIleArgLeu 247

QY 209 GTAGATCCCTGATCTGCATATCTTCCCGTTTCCTCATGATTTGAAGCCTCTCTTCT 268
::: :
Db 248 ValIleAspCysPheAlaIlePheLysGlnSerLysPheLeu----- 260
QY 269 TCCCTGATGACTTTGATCCCTCTGTTGTGTGAGAGTTGGACATGTTGATTACTG 328
::: :
Db 261 SerLeuAsnThrValAlaGlyIleProThrLeuAsp----- 272
QY 329 GTGGAAACAGCCACCATPACTGTAAATACACTCTTCTGACCAATGACTGACTGAG 388
::: :
Db 273 ValSerValSerProLeuHisGlyValAsnArgTyrIle-----Lys 286
QY 389 GAAGTGTGGAGGAGGTGCGCAAAAGACAGACCTCATY----- 430
::: :
Db 287 GluIleGluAspArgLeuLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 306
QY 431 -----CTCTCTTACCATCCGCTATCTTCTCGACCAACGAGACCGC 469
::: :
Db 307 ValIleAlaLeuGlyValLysLeuSerSerProGlyProValPheTyrLysGlnValArg 326
QY 470 ATAACTGGAAACATGGAAGAGCGCTGCTG----- 502
::: :
Db 327 ValGlyTrpAsnAsnArgLysPheThrMetLeuLysPheArgSerMetProValAspAla 346
QY 503 -----ATCCGGGCTCTGGAGACAGATC-----GCT 529
::: :
Db 347 GluAlaLysThrGlyAlaValTrpAlaArgProGlyGluAsnArgAlaThrArgPheGly 366
QY 530 ATCTACTCTCTCATACACCTATGATGCTGCGCCCGGCGGCTCAACACTGGTTGCT 589
::: :
Db 367 AlaPheLeuArgLysThrSerLeuAspIleLeuProGlnIleuLeuAsn-----ValLeu 384
QY 590 AAAGG-----CTTGGAGCTGTGACCTCCAGGCC-----ATACAT 625
::: :
Db 385 LysGlyAspMetSerLeuValGlyProArgProGluArgProAspPheValGluValPhe 404
QY 626 CCTTCAAGCTCCCACTAC----- 646
::: :
Db 405 LysAspGlnValProAsnTyrMetLysLysHisMetValLysAlaGlyIleThrGlyTyr 424
QY 647 -----CTTCAAGAGGAAACCCAGCTGATTCACCTT 682
::: :
Db 425 AlaGlnValAsnGlyTrpArgGlyAspThrAspLeuAsnArgGlyIleGlnHisAspLeu 444
QY 683 AACTACACCAA 694
::: :
Db 445 TyrTyrIleGln 448

RESULT 5
US-09-328-352-4482
; Sequence 4482, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4482
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4482

Alignment Scores:
Pred. No.: 0.0358 Length: 262
Score: 103.50 Matches: 62
Percent Similarity: 30.79% Conservative: 43
Best Local Similarity: 18.18% Mismatches: 113
Query Match: 3.71% Indels: 123
Gaps: 13

Alignment Scores:

Pred. No.:	0.285	Length:	588
Score:	97.00	Matches:	67
Percent Similarity:	38.61%	Conservative:	50
Best Local Similarity:	22.11%	Mismatches:	96
Query Match:	3.48%	Indels:	90
DB:	4	Gaps:	13

US-09-745-506-74 (1-1553) x US-09-328-352-7994 (1-588)

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QY 563 CCCAGGCGGTGAACACTGTTGGCTTAAGGCGTTGACTCTCAGGCCATA 622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 ProleuGlnleuAlaasnArgleuAlaSerArgleuValMetSerGlnMetaspIle 268
QY 623 CATCTCCCAAGCTCC-----ACTACCCCTACAGAGGGAACCAACCGA 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 SerGlnLysArgValProGlnAspGlyArgIleLysleuLysLeuSerLysAla 288
QY 668 GTAGAATTCACGTTAACTACACCCCAAGACCTG-----GACAAAGTCATG 712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 289 IleAspPheArgValAsnSerLeuProThrLeuPheGlyGlnLysLeuValIleuArgIle 308
QY 713 -----TCTGCACTGAAAAGAAATGACGGTGTCTGCTCATCTTTTCTGCT 760
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 LeuAspProSerSerAlaMetLeuGlyIleAspAlaLeu----- 321
QY 761 AGGACTGCTAATGAGAACAAACCGGATTAATCTCAATTTGCTCAGAAAGCTTGAG 820
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 322 -----GlyTyrGlnLysAsp-----GlnLysAlaLeuPhe 331
QY 821 CAGGTGCTGATTTCTTCCCGAACAACAATTATCAGAGACGAATTCGTCTCA 880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 -----MetGlnAlaLeuAspLysProGlnGlyMetLeuLeuIleThrGlyProThrGly 349
QY 881 CTGGAGAACCTTTGCTTCTACATCTGGAATGGACGGTTATGACACTGATGATCT 940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 350 SerGlyLysThrValSerLeuTyrThrGlyLeuAsnIleLeuAsnThr-----GlnSer 367
QY 941 GTCCTCCCTGGCAACCTGATGATGCAATTAAGAACCTTAATA-----CATCTCATATT 997
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 SerAsnIleSerThrIleGlnAspProValGlnIleAsnLeuGlnIleAsnGlnVal 387
QY 998 CGCTTACGCCCTTGGGGGAGAACCTTGAAGCTCAAGTCAAAAGTCGGCCCTGTGT 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 AsnValAsnProLysValGlyLeuThrPheAlaIleLeuLys----- 402
QY 1058 GCTGCTTGGGAGACGCTTCTGACAGGCTGTGAGGCTTACCTCAGAGGTGAG 1117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 403 -----SerPheLeuArg-----GlnAspProAspIleIleMetValGlyGln 416
QY 1118 ATGTCCCATCATGATCT-----TTGGATGCTGCTTCCCAAGTAATTAATGTC 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 IleArgAspLeuGlnThrIleGlnIleAlaIleLysAlaIleGlnThrGlnHisMetVal 436
QY 1166 ATCTCTCTGACACACGACAACTGACAGAGGCTTTCTTCTGACCTTCAGATATGCTG 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 MetSerThrLeuHisThrAsnSerAlaProGlnThrLeuThrArgLeuAsnMet----- 455
QY 1226 GATTTCTACTTGAGAAATAGATAAATTAATTCATACAGACGACGAGGACCTCTT 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 ----- 455
QY 1286 CAGGTGCTTAATTCGAGAAACATCAGATTAACATTCCTACAATTCAGTGTGATGCC 1345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 456 -----GlyValPro 458
QY 1346 AACTTAATTTTGAACATGAGTCACTGAGGACGTGTGCTTCAGAGAGTGTCTTGAGG 1405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 459 SerPheAsnIle-----AlaThrSerValAsnLeuValIleAlaGlnArgLysAlaArgArg 477
QY 1406 GATATCATCA 1414
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Db 478 LeucYsser 480

RESULT 9

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US-10-002-593-10
; Sequence 10, Application US/10002593
; Patent No. 6586198
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Brown, Nancy J.
; TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTING ENZYME INHIBITOR AND VASOPRESSIN RECEPTOR INHIBITOR ASSOCIATED ANGIOEDEMA
; FILE REFERENCE: Atty Docket No. 6586198 1242/48/2
; CURRENT APPLICATION NUMBER: US/10/002,593
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/244,524
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-002-593-10
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Alignment Scores:

Pred. No.:	0.289	Length:	493
Score:	96.50	Matches:	60
Percent Similarity:	35.23%	Conservative:	45
Best Local Similarity:	20.13%	Mismatches:	108
Query Match:	3.46%	Indels:	85
DB:	4	Gaps:	12

US-09-745-506-74 (1-1553) x US-10-002-593-10 (1-493)

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QY 446 CCTATCTCCGACCCATGAGCGCATTAACCTGGAACATGAGAGCGCCCTGGTATC 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 ProIleTyrAlaLeuGlnGlnAlaPheThrGlySerThrTrpGlnGlnLysValPro 40
QY 506 CGGGCTCTGGAGAACAGAGCTGATCTACCTCCATACAGCTTGAATGCTGCGGCC 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 -----SerGlyValArgSerGlnMetGlnLysGlnLysValPro 54
QY 566 CAGGCGCTC-----AACAACTGCTTGGCTTAAGGCTTGAGCT 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 55 ThrAlaValLeuLeuSerAlaLeuGlnGlnThrAlaTrpLeuPheAsn----- 70
QY 605 TGTACTCCAGGCCCATATCTCTCCAAAGCTCCCACTACCTCAGAGGGAACAC 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 71 -----LeuArgAlaSerAspIleProTyrAsnPro----- 80
QY 665 CGAGTAGAATTCAAAGCTTACTACACCCAGACCTGACAAAGCATGCTGCGAGTGA 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 -----PhePheTyrSerTyrThrLeuLeuThrAsp----- 90
QY 725 GGAATGACGCGTGTCTCTACCTTTCTTCTGCTAGAGCTGTAATGAGAACAAACA 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 -----SerSerIleArgLeuPheAlaAsnLysSerArgPheSerSerGlnThrLeuSer 108
QY 785 CGGATTAATCTGAATGTACTCAGAGAGGCTTGTATGACAGGTGATGATTTT----- 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 109 TyrLeuAsnSerSerCysThrGlyProMetCysValGlnIleGlnAspTyrSerGlnVal 128
QY 836 -----CTTCCCGGGAACAA 850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 ArgAspSerIleGlnAlaTyrSerLeuGlyAspValArgIleTrpIleGlyThrSerTyr 148
QY 851 CAACTTAATGAGAAAGCAAAATTCCTGCTACGAGAGGCTTGTCTTACATATCTGGA 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 ThrMetTyrLysIleTyrGlnMetIleProArgGlnLys----- 161
QY 911 ATGGAGCGTTATGACACCTGATGAATTCGTCTCCCTGCAACCATGATGATGATA 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 -----LeuValThrAspThrTyrSerProValMetMetThrLysAlaVal 176
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QY	AAAAGACAC-----CTAAATATCTCAATATCGCTTGAGCCCTGGAGTG	1015
Db	177 LysansserIysGluGlnAlaLeuLeuLysAlaSerHisValAlaGAspAlaValAlaVal	196
QY	1016 GGGAGA-----ACCTAAGAGCTCAAGTCAAAGTCGAGCCCTGTGCTGGTTCT	1066
Db	197 IleArgTyrLeuValTyrPLeuGluLysAsnValProLysGlyThrValAspLysPheSer	216
QY	1067 GGGAGACAGCTTCTGACAGGAGTGTCAGGCTGACCTTACACACAGTGAGATGTCGCAT	1128
Db	217 GlyAlaGluIleValAspLysPheArgLysGluGlnPheSerSerGlyProSer----	235
QY	1127 CATGATACTTGGATGCTGCTCCCAAGAAATAATGTCATCTCTGGAACACAGCAAC	1186
Db	236 PheGluThrIleSerAlaSer-----GlyLeuAsnAlaAlaLeuAlaHisTyrSerPro	253
QY	1187 ACTGAA-----CGAGGCTTCTCTTCTGACCTTCAGATGATGATGATGAT	1231
Db	254 ThrLysGluLeuAsnArgLysLeuSerSerAspGluMetTyrIleLeuAspSer	271

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RESULT 10
US-08-911-853-7
; Sequence 7, Application US/08911853
; Patent No. 6048710
; GENERAL INFORMATION:
; APPLICANT: Gerltse, Gijlsbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSSE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,853
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/699,092
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gjalster, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-911-853-7

Alignment Scores:
Pred. No.: 0.331 Length: 503
Score: 96.00 Matches: 62
Percent Similarity: 38.33% Conservative: 30
Best Local Similarity: 25.83% Mismatches: 61
Query Match: 3.44% Indels: 87
Db: 3 Gaps: 15

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OY	878	TCACGTAGAGAAAGCCT	-----TTGCCTCTA	-----CATACTGGAATGAGAGCGTTA	922
Db	252	ASmeuLurIrySpIroHISgIyIleIleuValThrGlyProThrgIySerGlyLysThr			271
OY	923	TGCACACTG	-----GATGAATCTGTCCTCCGACCAACATG		958
Db	272	ThrThreLyuValIaGlyLeuValThrLeuAsnSparSerArgAsnIleThrVal			291
OY	959	ATTATGTGCAATAAAAGACACACTAAACATATCTCATTTGCTTACGACCTTGGGGGTGGG			1018
Db	292	GLuSpproIleGlyLyrIyLeuGLu	-----GLYIleGly		303
OY	1019	AGACCTTAGAGTGTCAAGTCAAAATGTC	---GTGGCCCTGTGCTGTTCTTGAGACAGC		1075
Db	304	GLInThr	-----GLInValAsnProArgValAspMetThrPheAlaArgIlyLeuArg		320
OY	1076	GTTCGTGACGGGTGTGAGCGCTGACCTTATACCTCAGACGGTAGAGATGCCATCATGATCT			1135
Db	321	AlaIleLeuArgIAsnProAspValAlaMetValGlyIuIleArgAspGlnGluThr			340
OY	1136	TTGATGTGCTGCTCCCA	-----GGAATTAATGTCAATCCCTGTGACACACAGC		1183
Db	341	AlaAspIleAlaValGlnAlaSerLeuThrGlyHisLeuValIleuSerThrLeuHisThr			360
OY	1184	AACATGACAGCAGGCTTTCTTTCTGACCTTGACATATG	-----CTG		1225
Db	361	AsnSerAlaValGlyAlaValThrArgLeuValAspMetGlyValGluProPheLeuLeu			380
OY	1226	GATTCCTCACTGGAGCAATGAATAAATTTATTCATCAGAGACTGACAGAGGACCTCTT			1285
Db	391	SerSerSerLeu	-----LeuIlyValLeuAla	GLInArgLeuValAlaArgValLeu	396
OY	1286	CAGGTGTATATTATTCAGAAACATCAGAGATAA	-----		1318
Db	397	---CysValHisCysArgGluAlaIaArgProAlaIaIaGlyCysGlyLeuLeuGlu			415
OY	1320	-----CATTC	-----TACAAATCAGCTGAGTCCCAACTAAATTG		1355
Db	415	YLeuAspProHisSerGlnProLeuIleLyrHisAlaIySgIyCysPro	-----		431
OY	1358	TAACTATGAGTCAGTGGGAGCTGTGTCTTCAGAGAGTATGCTTCGAGGGATATCATCATTT			1411
Db	432	---	GLuCyS	-----	433
OY	1418	CCGGTTTGTATCTTATTCACCAATGTCTATAGCTCCGTAAGGTAACGTAATA			1475
Db	434	-----HisGlnGlnGlyLyrArg	-----GlyArgThrGlyIle		444

RESULT 11
 US-09-479-409-7
 ; Sequence 7, Application US/09479409
 ; Patent No. 6225106
 ; GENERAL INFORMATION:
 APPLICANT: Gerltise, Gylsbert
 APPLICANT: Quax, Wilhelmus J.
 TITLE OF INVENTION: EXPRESSION SYSTEM FOR AN
 TITLE OF INVENTION: EXPRESSION LEVELS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genecore International
 STREET: 925 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1013
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fastsoft for Windows Version 2.0.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/479, 409

FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/911,853
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaister, Debra J
 REGISTRATION NUMBER: 33,888
 REFERENCE/DOCKET NUMBER: GC361-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-846-7620
 TELEFAX: 650-845-6504
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 503 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-479-409-7

Alignment Scores:
 Pred. No.: 0.331 Length: 503
 Score: 96.00 Matches: 62
 Percent Similarity: 38.33% Conservative: 30
 Best Local Similarity: 25.83% Mismatches: 61
 Query Match: 3.44% Indels: 87
 DB: 3 Gaps: 15

US-09-745-506-74 (1-1553) x US-09-479-409-7 (1-503)

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QY 878 TCACTGGAGAGCCT-----TTGCTTCTA-----CATACTGGAATGGACGGTTA 922
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 AsnLeuArgLysProHisGlyIleIleLeuValThrGlyProThrGlySerGlyLysThr 271
QY 923 TGCACACG-----GATGAATCTCTCCCTCCGACACCATG 958
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 272 ThrThrLeuArgLysLeuValThrLeuAsnAspArgSerArgAsnIleLeuThrVal 291
QY 959 ATTGATCGAATAAAGACACCTAAACATATCTCATATTCGCTTACCCCTGGGGGGG 1018
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 GluAspProIleGlyLeuValThrLeuValThrLeuValThrLeuValThrLeuVal 303
QY 1019 AGAACCTTACAGCTCTCAAGTCAAGTC---GTGGCCCTGTGCTGCTTGGGACGAC 1075
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 304 GluThr-----GlnValAsnProArgValAspMetThrPheAlaArgGlyLeuArg 320
QY 1076 GTTCTCAGGGGTGTGAGGCTGACCTTACCTCAGAGTGCCATCATGATACT 1135
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 321 AlaIleLeuArgGlnAspProAspValValMetValGlyGluLeuArgAspGlnGluThr 340
QY 1136 TTGATGCTGCTCCCA-----GGAATAATGTCACTCTGTGAACACAGC 1183
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 341 AlaAspIleAlaValGlnAlaSerLeuThrGlyHisIleuValLeuSerThrLeuHisThr 360
QY 1184 AACACTGAACGAGGCTTCTTCTGACCTTGCAGATATG-----CTG 1225
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 AsnSerAlaValGlyAlaValThrArgLeuValAspMetGlyValGluProPheLeuVal 380
QY 1226 GATTCACACTGGAGAAATAAGATAATATATATCTTACAGACGTGACAGGACCTCTT 1285
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 381 SerSerSerLeu-----LeuGlyValLeuAla-GlnArgLeuValArgValLeu-- 396
QY 1286 CAGGTGTAATTTGAGAAACATCAGAGTAACA----- 1319
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 397 ----CysValHisCysArgGluAlaArgProAlaAspAlaAlaGluCysGlyLeuGlu 415
QY 1320 -----CATTC-----TACAATCAGCTGATGCCCACTTAATTTG 1357
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 yLeuAspProHisSerGlnProLeuIleuGlyHisAlaValGlyCysPro----- 431
QY 1358 TAAACATGAGTCACTGGGACTGTGTGCTTCCAGAGACTCTTCGAGGATCATCTTT 1417
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 432 -----GluCys----- 433

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QY 1418 CCGTTTGTAATCTTATTCACCAAGTGTCTACGCTGCTGAGTAAACGTGAATA 1475
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Db 434 -----HisGlnGlnGlyTyrArg-----GlyArgThrGlyIle 444

RESULT 12
US-09-479-453-7
; Sequence 7, Application US/09479453
; Patent No. 6313283
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelms J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-479-453-7

Alignment Scores:
Pred. No.: 0.331 Length: 503
Score: 96.00 Matches: 62
Percent Similarity: 38.33% Conservative: 30
Best Local Similarity: 25.83% Mismatches: 61
Query Match: 3.44% Indels: 87
DB: 4 Gaps: 15

US-09-745-506-74 (1-1553) x US-09-479-453-7 (1-503)
QY 878 TCACTGGAGAGCCT-----TTGCTTCTA-----CATACTGGAATGGACGGTTA 922
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 AsnLeuArgLysProHisGlyIleIleLeuValThrGlyProThrGlySerGlyLysThr 271
QY 923 TGCACACG-----GATGAATCTCTCCCTCCGACACCATG 958
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 272 ThrThrLeuArgLysLeuValThrLeuAsnAspArgSerArgAsnIleLeuThrVal 291
QY 959 ATTGATCGAATAAAGACACCTAAACATATCTCATATTCGCTTACCCCTGGGGGGG 1018
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 GluAspProIleGlyLeuValThrLeuValThrLeuValThrLeuValThrLeuVal 303
QY 1019 AGAACCTTACAGCTCTCAAGTCAAGTC---GTGGCCCTGTGCTGCTTGGGACGAC 1075
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 304 GluThr-----GlnValAsnProArgValAspMetThrPheAlaArgGlyLeuArg 320

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US-08-681-151-3
; Sequence 3, Application US/08681151
; Patent No. 5869637
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Bandman, Olga
; APPLICANT: Braxton, Scott Michael
; APPLICANT: Goll, Surya
; TITLE OF INVENTION: A NOVEL HUMAN KALLIKREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,151
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-007405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TEXAS:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 638 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 205011
; US-08-681-151-3

Alignment Scores:
Pred. NO.:          0.487           length:      638
Score:              95.00           Matches:     78
Percent Similarity: 33.24%           Conservative: 35
Best Local Similarity: 22.94%         Mismatches: 112
Query Match:        3.41%            Indels:      116
DB:                  2                Gaps:        15

US-09-745-506-74 (1-1553) x US-08-681-151-3 (1-638)
QY 143 GTCTCGGAAAAGGCCTGAAGTGGCAGCTGAATGAGCATGATGACTGCCACAGACAGTC 2022
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Db 167 LeuLeuLysArgSerSerSerIylthr-----ProThrSerile 179
QY 203 CGGTGTGAGAGATTCCCTGATCGCAATTCNCCGTTCTTCATGATGATTGGAAGGCTTC 262
   :: |||||||:::||||| |
Db 180 LysProlValAsnIleValSerIylPheSerLeuLysSerCysAlaIleuSerGIulle 199
QY 263 CTTCCTTCCTTGAAAGACTTTCGATCCCTCTGCTTGTGAGAGTTGGGACAATGTTGGA 3222
   :::::: ||| :::|||||::: |||||
Db 200 GlyCysPrometAspIlePheGlnHisPheAlaPheAlaAspLeu-----AsnValSer 217
QY 323 TTACTGGTGAACCAAGCCA-----CCACATACT 3522

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DB 218 GlnValValThrProAspAlaPheValCysArgThrValGlySerThrPheHisProAsnCys 237
:::|||||
OY 353 GTAATACACTCTTCTCGAACAATGACCCTGCAGTAGAGAGTGAGGAGGTGGTCGAA 412
::: |||||:::
Db 238 LeuPhePheThrPheTythrAsnGluTrpLeuThrGlnSerGlnArgAsnValCysPhe 257
413 AAGAAGCAGCACTCATTTCTCTCCATCCGCCCTTATCTTCGACCAACCATGAMGCCATA 472
|||
Db 258 LeuIysThrSerLysSerGlyArgProSerProIleIleGln----- 272
473 ACCTGGAAACATGGGAAGAGCGGCTGTATCCGGGCTCTGGGAACACAGATCGGTATC 532
273 -----GluAsnAlaValSerGly 278
OY 533 TACTCTCCCTATACAGCCTATGATGCTGCGCCCCAGGCGCACAACAATGGTTGGCTAAA 592
||||| ||| |||:::
Db 279 TyriserLeuPheThrCysArgLysAlaArgProIu----- 290
593 GGCGTTGGAGCTGTACCTCCAGGCCATACATCCCTTCCAAGACTCCCAACTACCTACA 652
291 -----ProCysHisPheLysIleTyrseryValAlaPhe 302
OY 653 GAGGGAACACCAAGTAAGAATTCAAGATTACACCCCAAGACTGGACAA---AGT 708
||||| ||| |||:::
Db 303 GluLysGlu-----GluLeuAsnAlaThrPheValGlnGlyAlaAspAlaCysGln 319
709 CATGTCGCACGTGAAGAAGAAATGACGGGTGTTCTGCACTCTTTCTTCTGTACGACTGG 768
|||:::
Db 320 GluThrCysThrLys-----ThrIleArgCysGlnPhePhe----- 331
769 TAATGAGAACMAACACGAGATTAACTGAAATTGACTCA----- 807
332 -----ThrTyriserLeuLeuProGlnAspCysLys 341
OY 808 ---GAGGCTTGTATGACAGGTGTAGATTTTCTTCCCGGACAAACAACCTTATTCGAA 864
||||| |||
Db 342 AlaGlnGlyCysLysCysSerLeuArg-----LeuSerThr 353
865 GAGGGAAT-----TGTGTCACGTGAGAGAACCTTTGCTCTACATACGTGGAATGGAGC 918
|||||:::
Db 354 AspGlySerProThrArgLierHtyrGlnAlaGlnLysSerGlyTyrsr-LeuAr 373
919 GTTATGACACATGATGATGATCTGTCTCCCTGGAACACCATGATTGCAATAAAAAGACA 978
|||||::: ||||| |||
Db 373 GluEncybelysValValGlnUserSerAspCysThrThylsalle----- 387
979 CCTAAACATATCATATTCGCTTAGCCCTTGGSGGGGAGAACCTTA----- 1027
388 -----AsnAlaArgIleValGlyGlyThrAsnSerSerLeuGlyGluTrpr 403
1028 -----CAGTCTCAAGTCMAAGTCGTGGCC-----CTGTGCTGTGTTCT 1066
403 OTPrGlnValSerLeuGlnValLysLeuValSerGlnAsnHisMetCysGlyLysr 422

RESULT 15
US-09-134-001C-5218
Sequence 5218, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelte-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GPC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5218
LENGTH: 804

TYPE: PR1
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5218

Alignment Scores:

Pred. NO.:	0.559	Length:	804
Score:	95.00	Matches:	72
Percent Similarity:	33.81%	Conservative:	69
Best Local Similarity:	17.27%	Mismatches:	128
Query Match:	3.41%	Indels:	148
DB:	4	Gaps:	16

US-09-745-506-74 (1-1553) x US-09-134-001C-5218 (1-804)

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QY 266 TCCTTCCTGGAATGACCTTGACATCCCTCGTTGCTGAGAGTGGACATGTTGATTA 325
    |||||::: ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 84 SerSerValTyrAsp---AlaMetValArgLeuSerGlnAspThrPlysLeuArgHleVal 102
QY 326 CTGCTGGAA-----CCAGCCGACCATACCTGTAAT 358
    |||::: ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 103 LeuIleGluMetHisGlyAsnAsnGlySerIleAspAsnAspProProAlaAlaMetArg 122
QY 359 ---ACACTCTTCCTGACCAATGACCTGACATGAGAGATGAGAGAGTGTGCAAAAG 415
    |||||::: ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 123 TyrThrGluAlaIleAspSerGlnLeuSerGlnGluLeuLeuArgAspIleAsnLysGlu 142
QY 416 AAGCAGACCTCATCTCTCTCTACCATCCGCTATCTTCGACCCATGAGAGCGCATTAAC 475
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 143 ThrValSerPheIleProAsnTyrAspAspThrThrLeuGluPromet----- 158
QY 476 TGGAAACATGGAAGAGCGCTGTGATCCGGCTCTGGAAGACAGAGTGGTATCTAC 535
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 159 -----ValLeuProAlaArgPheProAsnLeuLeuIleAsnGlySerThrGlyIleSer 176
QY 536 TCT-----CCTCATACA----- 547
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 177 SerGlyTyrAlaThrAspIleProProHisAsnLeuAlaGluValIleGlnGlyThrLeu 196
QY 548 GCCTATGATGCTGCCGCCAGGCGGTCAACAACATGCTGTTGCTAAAGGCTTGAGCTTGT 607
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 197 LysTyrIleAspGlnProAspIleThrIleAsnGlnLeuMetLysTyrIle----- 213
QY 608 ACCCTCAGGCCCATCATCTCTCCAAAGCTCCCAACTACCTACGACAGAGGAAACCAACGA 667
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 214 -----LysGlyProAspPheProThrGlyGly----- 222
QY 668 GTAGATTCAACGTTACTACACCCAGACCTGGAACAAATCATGTCTGCAGTGAAGA 727
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 223 -----IleIleGlnGly 226
QY 728 ATTGACGGTGTTC----- 742
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 227 IleGlnGlyIleLysAlaIleArgIleuThrGlyLysGlyValIleValIleArgSerArg 246
QY 743 GTCACTTCTTTTTCGTAGAGCTGTATAGGAA-----CAAAACGGATTATCTG 796
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 247 ValAspGluGluProLeuArgSerGlyArgLysGlnLeuIleValThrGluIleProTyr 266
QY 797 AATTGTACTAGAGAGCTTTGATGAGAGTGTAGATTTCTTCCGGAACAACAACATT 856
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 267 GluValAsnLysSerSerLeuValLysArgIleAspGluLeuArgAlaAspLysLys--- 285
QY 857 TATCAGAAAGCAGAAATCTGTCACTGGAAGACCTTGTCTACATACCTGAATGGGA 916
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 285 ----- 285
QY 917 CGGTTATGCACCTGAGGAATCTGTCTCCCTGGCAACCATGATGATGAATAAAGA 976
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 286 -----ValAspGlyIleValGluValArgAspGluThrAspArg----- 298
QY 977 CACCTAAACATATTCGCTATGCGCTTACGCTGGGGTGGGAGAACCTTAGAGTCTCAA 1036
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 299 -----ThrGlyLeuArgIleAlaIleGluLeuLysLysAspAlaAsnSer--- 313
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QY 1037 GTCAAGCTCGTGCCCTGTGTGTCTGTGTTTGAGGACAGCGTTCTGCAGGCTGTGAGCT 1096
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 314 -----GluSerIleLysAsn 318
QY 1097 GACCTTACCTCACAGGTGAGATG-----TCCATCATGATACTTGTGATGCTGTCC 1150
    |||||::: ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 319 TyrLeuTyrIlyAsnSerAspLeuGlnIleSerTyrAsnPheAsnMetValAlaIleSer 338
QY 1151 CAAAGAAATTAATGTCATCTCTGTGAACACAGCAACAGTGAAGCGCTTCTTCTGAC 1210
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 339 GluGly-----ArgProLysLeuMetGly 346
QY 1211 CTTGAGATATAGCTGATCTTCATCTTGAGAGATAAGATAATATATCATCATCAGAGACT 1270
    |||||::: ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 347 LeuArgGluIleIleGluSerTyrLeuAsnHisGlnIleGluValIleThrAsnArgThr 366
QY 1271 GACAGGACCCCTTCAGGTGTGTAAATTCAGAAACATCAGATTAACATTCCTACAA 1330
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 367 ArgTyrAsp-----LeuGluGlnAlaGluLysArgMetHisIleVal 380
QY 1331 ATCAGCTGAGATGCCCACTTAATTTGTACATGATCAGTGGAGCTGTG 1381
    ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 381 GluGlyLeuMetLysAlaLeuSerIleLeuAspGluValIleAlaLeuIle 397
```

Search completed: August 22, 2003, 14:07:00
Job time : 46 secs